

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

1-22. (cancelled)

23. (currently amended) A purified HIV-1 variant virus,
wherein said HIV-1 variant virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level to from HIV-1_{BRU} by from 9.8 to 12% in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein,
wherein the HIV-1 variant virus binds antibodies in AIDS patient sera,
said antibodies binding specifically to the virus designated HIV-1_{MAL} deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641,
wherein the genetic structure of said HIV-1 variant is 5'-LTR-gag-pol-vif-vpr-tat-rev-vpu-env-nef-LTR-3', and
wherein the nucleic acid of said HIV-1 variant virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe comprising~~ the genomic cDNA of HIV-1_{MAL} as shown in Figures 7A-7I over its entire length; and
said LAV_{MAL} virus contains at least one direct sequence repeat.

24. (cancelled)

25. (currently amended) The HIV-1 variant virus of claim 23, wherein the nucleic acid of said HIV-1 variant virus can be detected by hybridization with a ~~DNA probe comprising~~ a restriction enzyme fragment of the cDNA of HIV-1_{MAL}, and wherein the restriction enzyme is selected from the group consisting of *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HincII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*.

26-43. (cancelled)

44. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Env sequence of HIV-1_{MAL} as shown in Figure 3.

45. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Gag sequence of HIV-1_{MAL} as shown in Figure 3.

46. (previously presented) The HIV-1 variant virus of claim 23, wherein the virus has the Pol sequence of HIV-1_{MAL} as shown in Figure 3.

47. (cancelled)

48. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level to ~~from~~ HIV-1_{BRU} ~~by from 0.8 to 12%~~ in the entire Gag protein, from

92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~
in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the
COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM)
under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5'-LTR-gag-pol-vif-vpr-tat-rev-
vpu-env-nef-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent
hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe~~
~~comprising~~ the genomic cDNA of the virus deposited at the COLLECTION
NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641
over its entire length; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the
restriction map shown in Fig. 1.

49. (previously presented) The purified human immunodeficiency virus
designated LAV_{MAL} of claim 48, wherein the genome of LAV_{MAL} has the restriction
map shown in Fig. 1.

50. (currently amended) A purified human immunodeficiency virus
designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level to from HIV-1_{BRU} ~~by from 9.8 to 12%~~ in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the
COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM)
under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to ~~a DNA probe comprising~~ the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641 over its entire length; and

said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 1 to 530; 34-530; and 531-877.

51. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level ~~to from~~ HIV-1_{BRU} ~~by from 9.8 to 12%~~ in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to a ~~DNA probe~~ comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641 over its entire length; and

~~said LAV_{MAL} virus comprises a protein or glycoprotein encoded by at least one of the following LAV_{MAL} cDNA sequences of Fig 3E: 37-130, 211-289, 488-530, 490-620, and 680-700~~ said LAV_{MAL} virus contains at least one direct sequence repeat.

52. (currently amended) A purified human immunodeficiency virus designated LAV_{MAL}, wherein

said LAV_{MAL} virus is from 88 to 90.2% identical ~~differs~~ at the amino acid sequence level ~~to from~~ HIV-1_{BRU} ~~by from 9.8 to 12%~~ in the entire Gag protein, from 92.3 to 94.5% ~~5.5 to 7.7%~~ in the entire Pol protein, and 78.3 to 79.3% ~~20.7 to 21.7%~~ in the entire Env protein;

the HIV-1 variant virus binds antibodies in AIDS patient sera;

said antibodies binding specifically to the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641;

the genetic structure of said LAV_{MAL} virus is 5-LTR-*gag-pol-vif-vpr-tat-rev-vpu-env-nef*-LTR-3';

the nucleic acid of said LAV_{MAL} virus can be detected by stringent hybridization (50% formamide, 5X SSC, at 42°C, for 12-16 hours) to ~~a DNA probe comprising the genomic cDNA of the virus deposited at the COLLECTION NATIONALE DES CULTURES DE MICRO-ORGANISMES (CNCM) under No. I-641~~ over its entire length, ~~or a restriction enzyme fragment thereof, wherein the restriction enzyme is selected from at least one of the group consisting of~~ *AvaI*, *BamHI*, *BglII*, *EcoRI*, *HinII*, *HindIII*, *KpnI*, *NdeI*, *PstI*, *SacI*, and *XbaI*; and

the genome of said LAV_{MAL} virus comprises at least one restriction site of the restriction map shown in Fig. 1.

53. (New) The purified HIV-1 variant virus of claim 23, wherein the direct repeat is perfectly conserved.

54. (New) The purified HIV-1 variant virus of claim 23, wherein the direct repeat contains one or two point mutations.

55. (New) The purified HIV-1 variant virus of claim 23, wherein the direct sequence repeats comprise at least one of QQAAAA in HIV-1_{MAL} Gag, RAEP in HIV-1_{MAL} ORF F, DAVSQ in HIV-1_{MAL} ORF F, AVNGT in HIV-1_{MAL} Env, and DNS HIV-1_{MAL} Env.

56. (New) The purified HIV-1 variant virus of claim 23, wherein the direct sequence repeats comprise all of QQAAAA in HIV-1_{MAL} Gag, RAEP in HIV-1_{MAL} ORF F, DAVSQ in HIV-1_{MAL} ORF F, AVNGT in HIV-1_{MAL} Env, and DNS HIV-1_{MAL} Env.